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FIG. 1

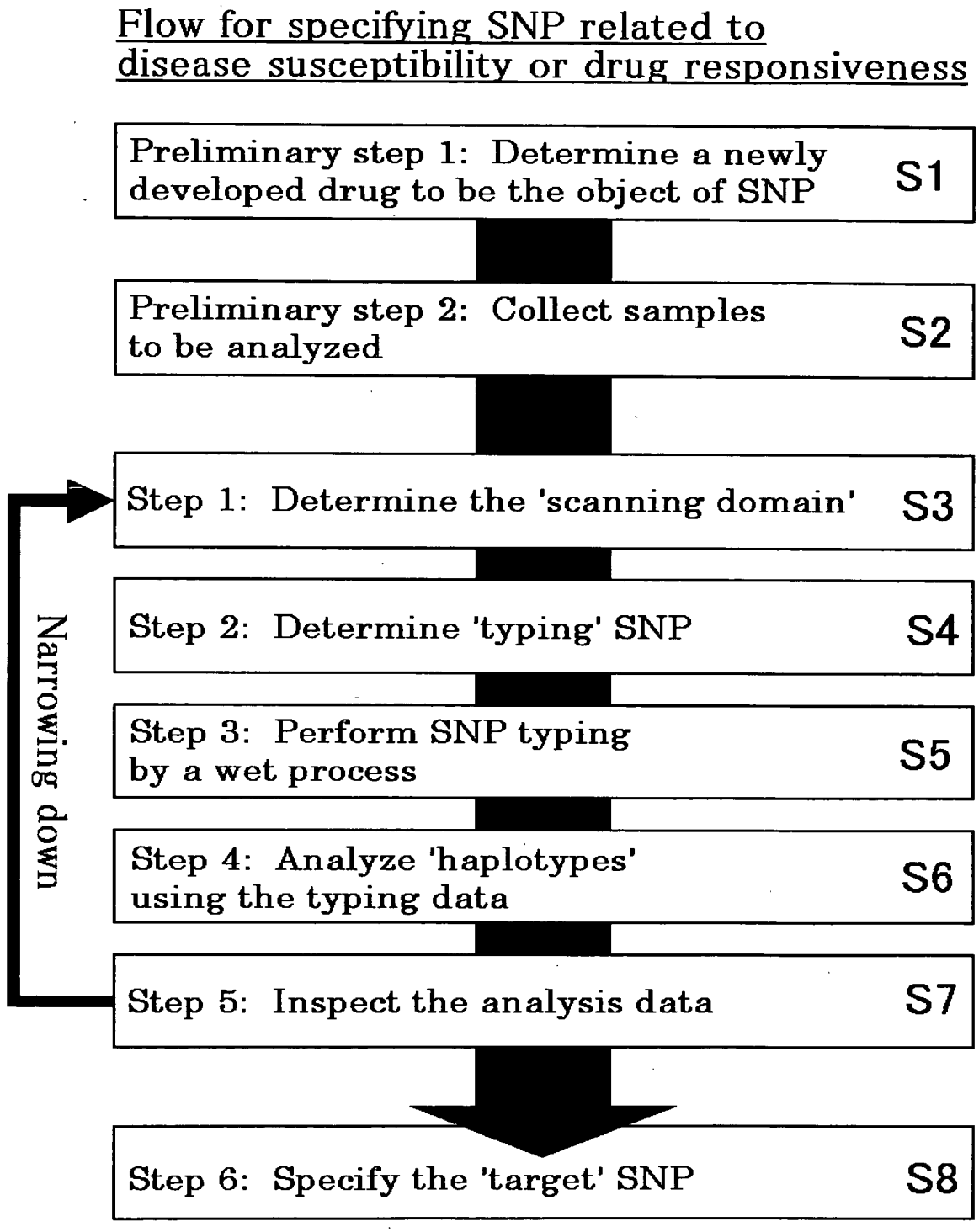

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FIG. 2

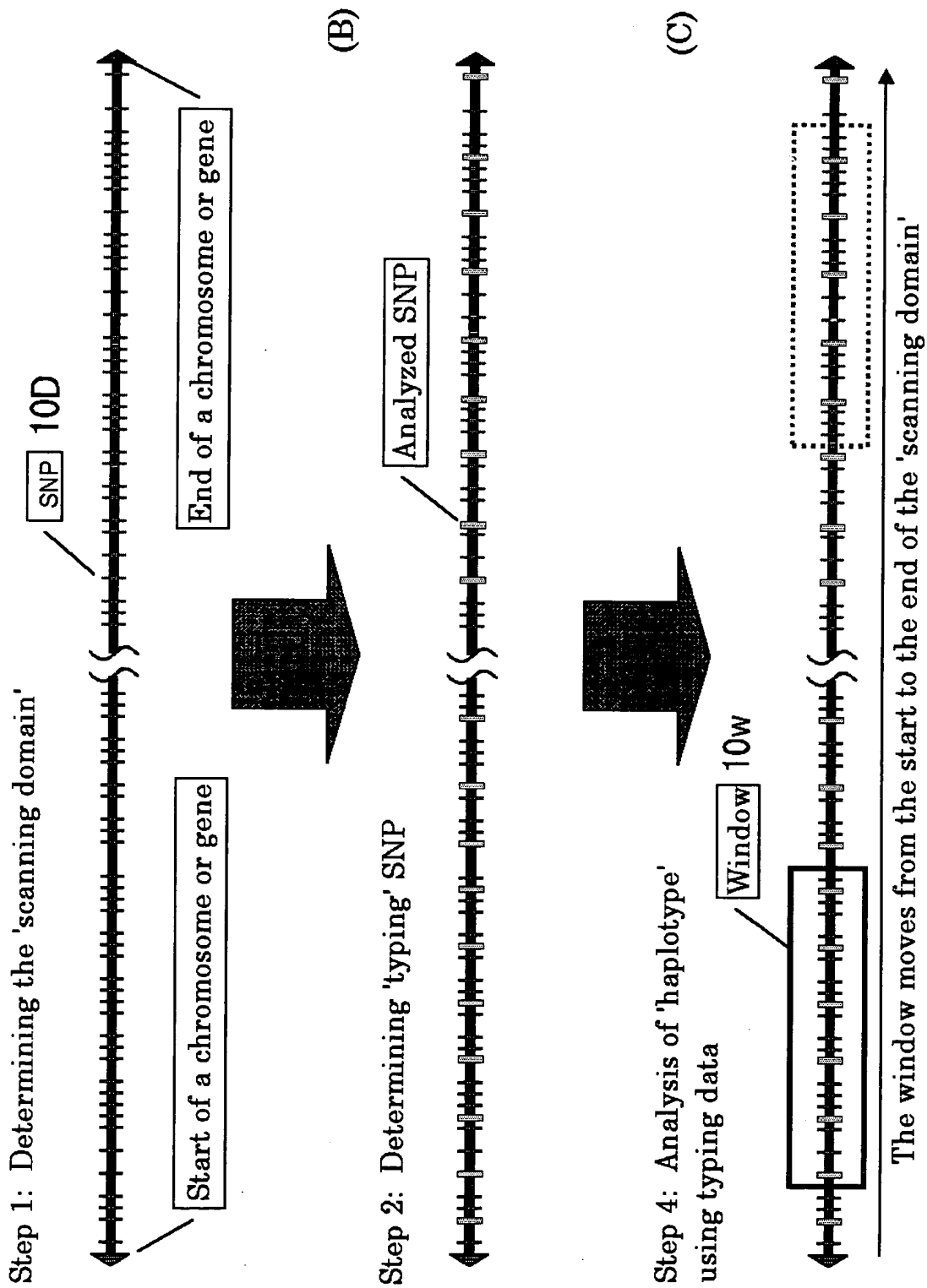

FIG. 3

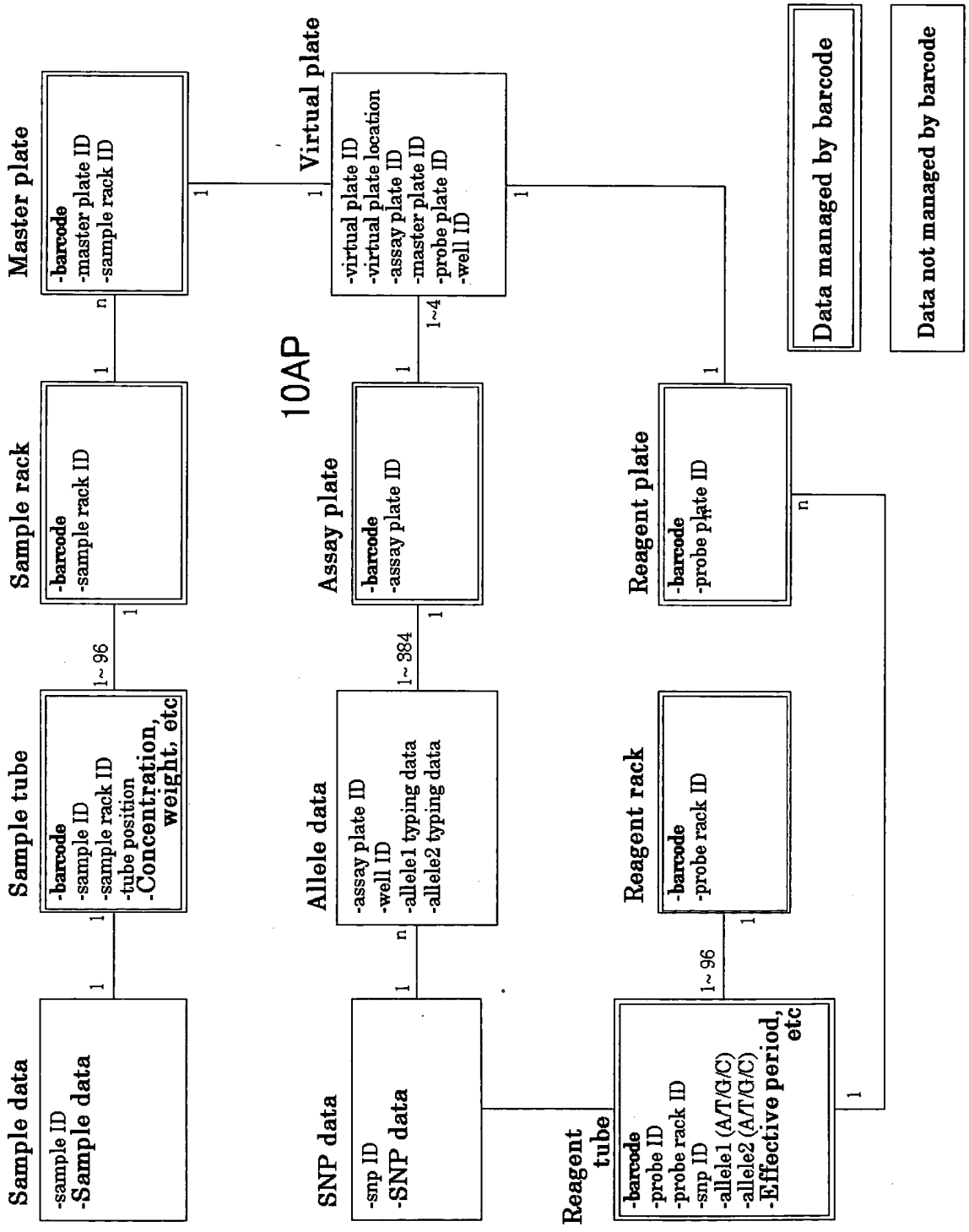
Master plate
-barcode
-master plate ID
-sample rack ID
Virtual plate
-virtual plate ID
-virtual plate location
-assay plate ID
-master plate ID
-probe plate ID
-well ID
Data managed by barcode
Data not managed by barcode
Sample rack
-barcode
-sample rack ID
10AP
Assay plate
-barcode
-assay plate ID
Reagent plate
-barcode
-probe plate ID
Sample tube
-barcode
-sample ID
-sample rack ID
-tube position
-Concentration, weight, etc
Allele data
-assay plate ID
-well ID
-allele1 typing data
-allele2 typing data
Reagent rack
-barcode
-probe rack ID
Sample data
-sample ID
-Sample data
SNP data
-snp ID
-SNP data
Reagent tube
-barcode
-probe ID
-probe rack ID
-snp ID
-allele1 (A/T/G/C)
-allele2 (A/T/G/C)
-Effective period, etc
1
n
1~96
1~384
1~4

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FIG. 4

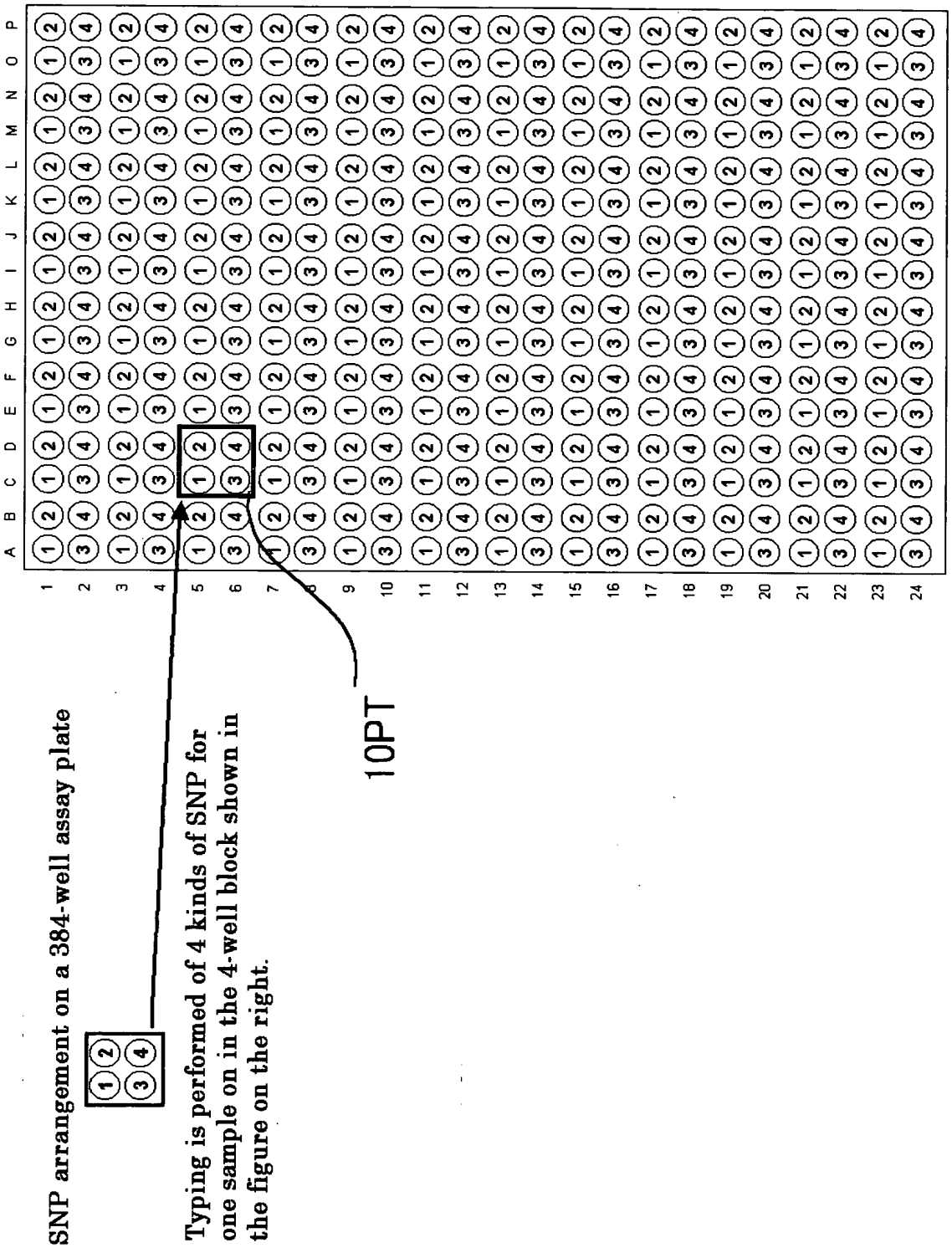


FIG. 5

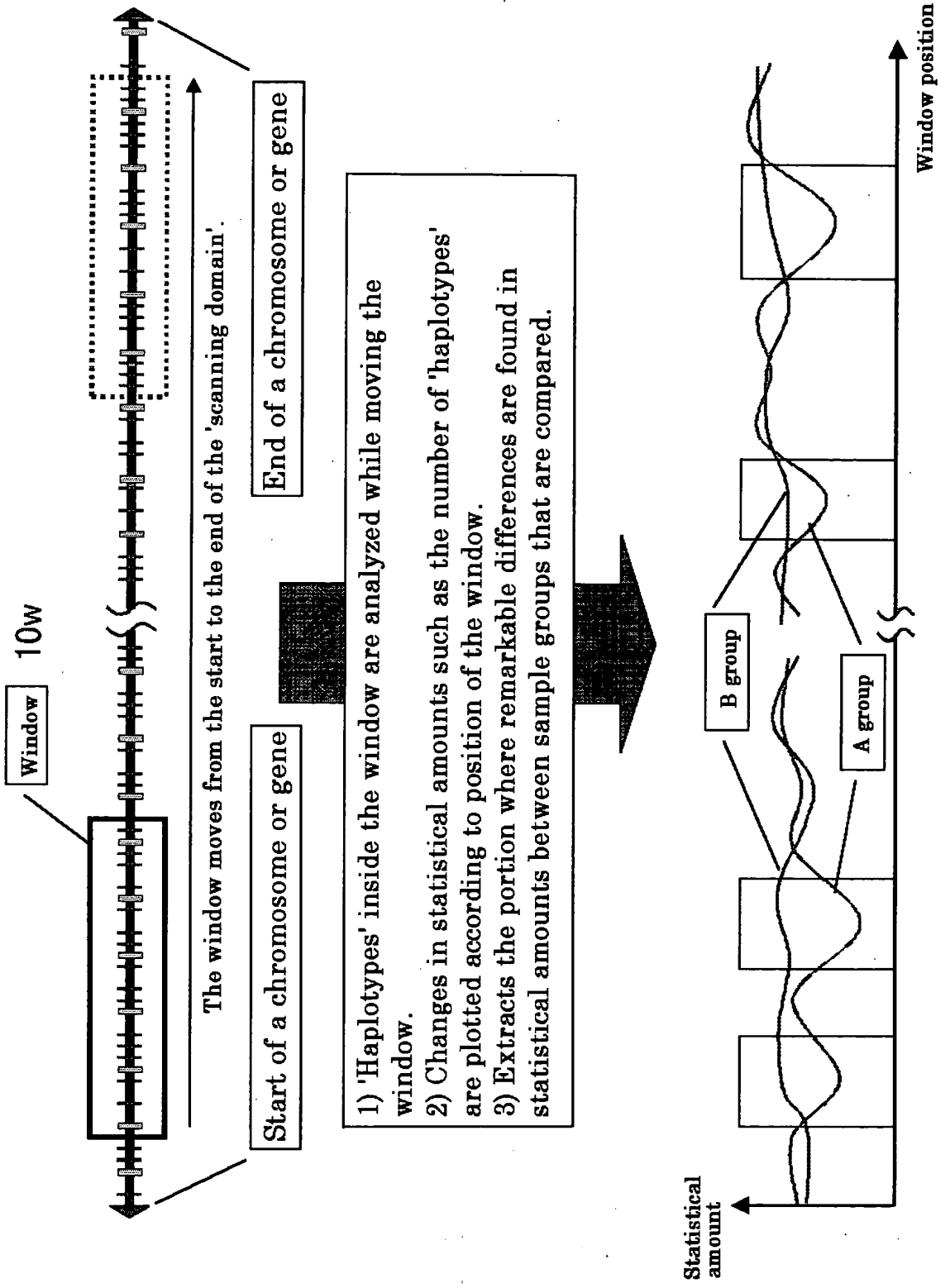

Window
10w
The window moves from the start to the end of the 'scanning domain'.
Start of a chromosome or gene
End of a chromosome or gene
1) 'Haplotypes' inside the window are analyzed while moving the window.
2) Changes in statistical amounts such as the number of 'haplotypes' are plotted according to position of the window.
3) Extracts the portion where remarkable differences are found in statistical amounts between sample groups that are compared.
B group
A group
Statistical amount
Window position

FIG. 6

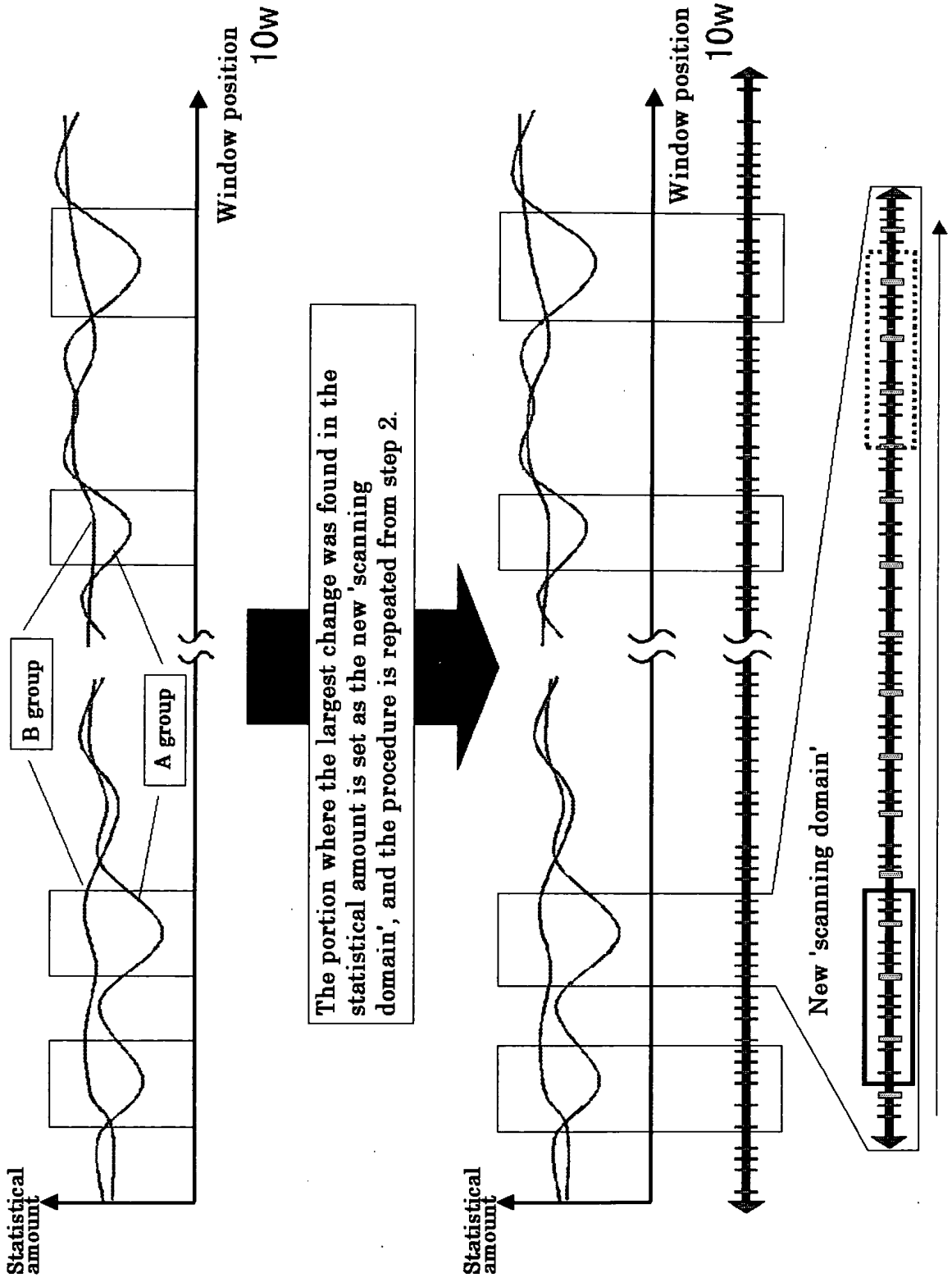
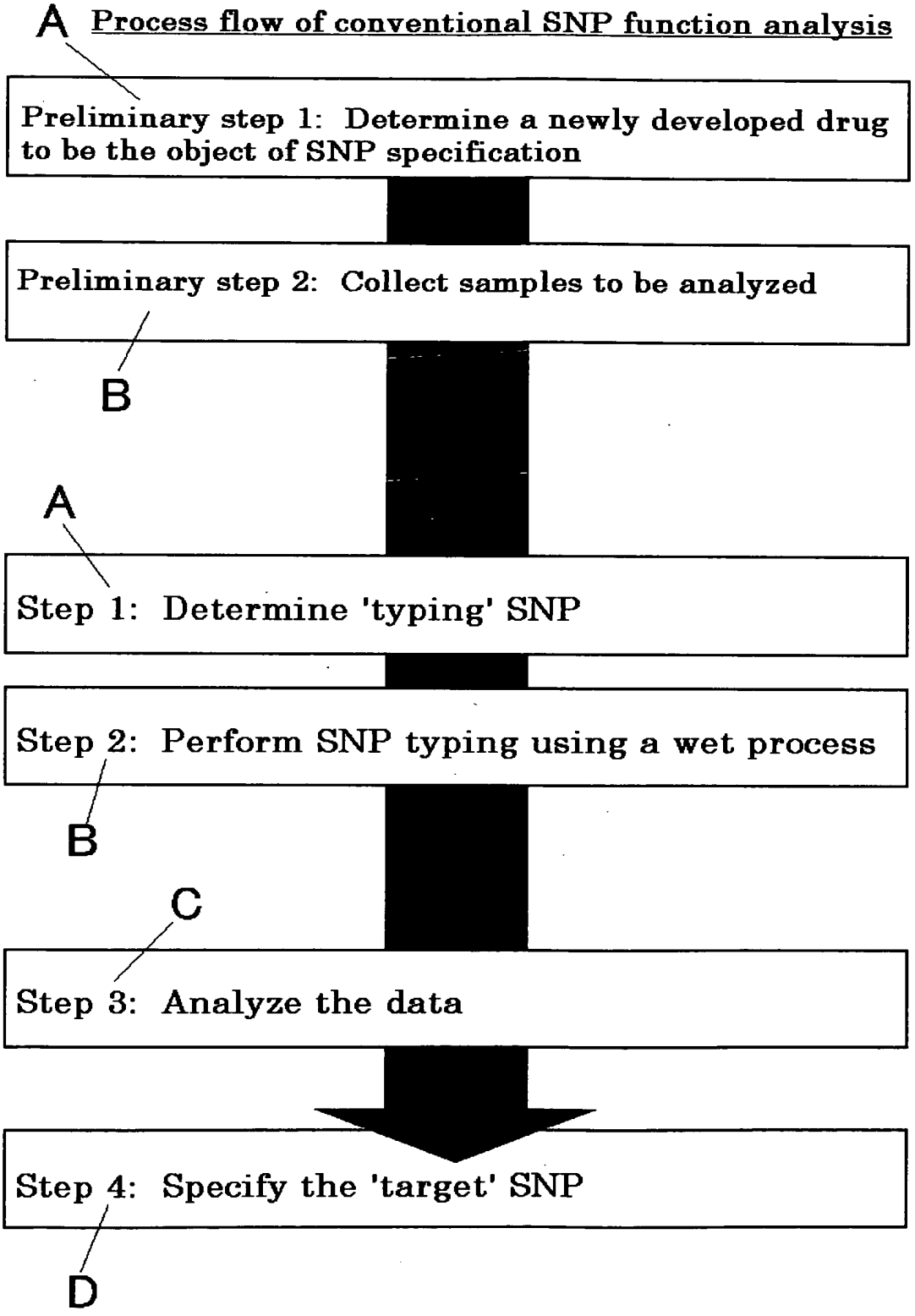

Window position
10w
B group
A group
Statistical amount
The portion where the largest change was found in the statistical amount is set as the new 'scanning domain', and the procedure is repeated from step 2.
Window position
10w
New 'scanning domain'
Statistical amount

FIG. 7


A Process flow of conventional SNP function analysis
Preliminary step 1: Determine a newly developed drug to be the object of SNP specification
Preliminary step 2: Collect samples to be analyzed
B
A
Step 1: Determine 'typing' SNP
Step 2: Perform SNP typing using a wet process
B
C
Step 3: Analyze the data
Step 4: Specify the 'target' SNP
D

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Explanation of reference numbers

10AP	Assay plate
10D	SNP
10PT	4 divisions
10w	Window

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